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Editorial: Molecular markers of plant adaptation to multiple environmental stressors

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Editorial on the Research Topic

Molecular markers of plant adaptation to multiple environmental stressors

Environmental stressors impair plant growth, cause shifts in the root microbiome community, and alter the root exudate composition (Ali et al., 2022; Chai and Schachtman, 2022). Among beneficial microorganisms, rhizobia and arbuscular mycorrhizal fungi (AMF) improve plant tolerance to abiotic stress by modulating water uptake, nutrient assimilation, the antioxidative response, and photosynthetic performance (Ali et al., 2023). While the effectiveness of environmentally friendly approaches to preserving soil fertility is still emerging, it appears that their application is a suitable replacement for conventional agriculture. The aim of this Topic was to elucidate the internal plant mechanisms provoked by symbiotic interactions that may reprogram molecular and metabolic adaptive responses to environmental requirements. Among the contributions, Pree et al. presented new possibilities for exploring the interconnection between root hairs, rhizopines, and the root microbiome when coping with stressful situations.

Rhizopines are specialized root exudates that attract N-fixing bacteria, whereby certain groups of exudate compounds are destined for specific bacteria. Creating genetically engineered cereals with the ability to synthesize specific rhizopine groups could be an excellent alternative for preserving soil fertility. The secretion of rhizopines promotes the colonization of the rhizosphere by various microbiome communities, inducing root hair genesis and root plasticity. In this regard, barley so far has demonstrated the highest potential among all cereals. The composition of root exudates consists of diverse combinations of primary and secondary metabolites that may vary according to resource availability and environmental conditions. Bioactive molecules in root exudates determine the composition and variability of microbial and fungal root assemblages. In leguminous plants, flavonoid-rich rhizopins attract N-fixing bacteria more efficiently; however, in non-legumes, they may also influence the establishment of non-symbiotic diazotrophs in the root microbiome community. This opens new perspectives for the exogenous addition of

flavonoids in shaping root growth and fitness. Demands in growth conditions necessitate the modulation of auxin homeostasis, which controls root hair outgrowth. In cereals (e.g., barley) and *A. thaliana*, the focus is on understanding the mode of action of conserved regulatory pathways involved in auxin balancing. In barley, the β -expansin protein HvEXPB7 controls root hair development and contributes to drought tolerance. Root systems and root hair outgrowth can be monitored directly *in situ* using non-destructive imaging tools, such as minirhizotrons. Minirhizotron phenotyping has the potential to elucidate root plasticity and root hair-N₂-fixing bacteria interactions to minimize the utilization of synthetic N fertilizers.

The successful deployment of AMF-based products has consistently been challenged by what is often termed the Phosphate Paradox. Lucic-Mercy et al. provided a compelling demonstration that this paradigm is not immutable. By employing an innovative strategy, the authors successfully generated an AMF phenotype that is capable of partially bypassing the repressive effects of high phosphorus, thus paving the way for a truly resilient symbiont suitable for modern agricultural demands. The striking finding of this study is that inoculation with the RiQS81-Pi+ phenotype restored the high induction levels of CmSTR1, CmSTR2, CmBCP1a, and CmBCP1b in melon roots, even under high phosphorus conditions. This molecular restoration is the strongest evidence yet that the adapted fungus provides sufficient benefit to overcome the host plant's intrinsic Pi-sensing repression. The implications of this study are profound for basic research, inoculum production, and global agricultural sustainability. The study validates the strategy of directed fungal evolution as a powerful tool for generating new, commercially relevant traits, shifts the research focus from finding naturally occurring Pi-tolerant strains to actively creating them in the laboratory, and demonstrates that the improved propagule production ratios of the RiQS81-Pi+ lineage under high P suggest this adaptation is durable and scalable over subsequent generations. These findings bring AMF products closer to the goal of being reliable, high-performance inputs compatible with the current realities of intensive crop management.

Legume-rhizobium symbiosis is one of nature's most sophisticated nutrient exchange systems. In this symbiotic association, rhizobia fix atmospheric nitrogen within root nodules and return ammonium to the host plant. However, this process must be tightly regulated to match the plant's fluctuating nitrogen demand and environmental conditions. Martin et al. demonstrated these regulatory dynamics using a split-root experimental design. The authors exposed one-half of the *Medicago truncatula* root system, which was inoculated with *Sinorhizobium medicae* md4, to osmotic stress via polyethylene glycol (PEG). Then, they compared the results with those of the other half of the inoculated root system that was not exposed to stress. The results revealed a rapid and localized inhibition of nitrogen fixation under osmotic stress, which suppressed nitrogen fixation and triggered a systemic compensatory response in root nodules without stress. Root nodules distant from the stress site exhibited enhanced

development and increased sucrose allocation, while root nodules without stress showed plant systemic adjustment to maximize symbiotic efficiency. Under osmotic stress, root nodules showed a strong transcriptomic reprogramming through the overexpression of gene families related to nodule cysteine-rich peptides, gastrin-releasing peptide, core histones, leghemoglobins, SWEET sucrose transporters, and nodulin genes. Key transcripts involved in rhizobial recognition and infection, including *MtNPL*, *MtRPG*, *MtLYK10*, *MtDMI3*, *MtNSP2*, *MtEFD*, and *MtEFD2*, were differentially expressed under PEG treatment. AMF association establishes a mutualistic association with plant roots and benefits each other to grow and survive under abiotic stresses. AMF colonizes the root cortex and facilitates nutrient exchange by developing an arbuscular structure in the plant root. It facilitates plants with nutrient and water uptake and, in return, receives photosynthetically derived carbon compounds. Gao et al. observed metabolic and transcriptional reprogramming in AMF symbiosis in *Manihot esculenta* Crantz. AMF inoculation in *Manihot esculenta* roots showed the differential accumulation of metabolites associated with nitrogen assimilation and cellular metabolism, including 5-aminolevulinic acid, L-glutamic acid, and lysoPC 18:2. The authors reported the differentially expressed genes related to nutrient transport, hormone signaling, sugar metabolism, and symbiosis signaling pathways as a result of AMF inoculation.

The four articles in this Research Topic introduce the scientific community to advanced techniques, including transcriptomic reprogramming, short-term cultivation of highly adapted phosphorus fungi, hormonal regulation, root exudate metabolomic analysis, phenotyping of the root system, and root hair development. All of these are promising tools for efficient N uptake and excellent solutions against the overuse of synthetic N fertilizers, which are a significant source of greenhouse gas emissions.

Author contributions

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